

=> file ca

=> s (trnI or trnA)/ab,bi

L1 22744 (TRNI OR TRNA)/AB,BI

=> s l1 and (chloroplast?)/ab,bi

27670 (CHLOROPLAST?)/AB

32945 (CHLOROPLAST?)/BI

L2 768 L1 AND (CHLOROPLAST?)/AB,BI

=> s l1 and (gene or genes or vector? or plasmid? or cdna? or transgenic?)/ab,bi

L3 6707 L1 AND (GENE OR GENES OR VECTOR? OR PLASMID? OR CDNA? OR TRANSGENIC?)/AB,BI

=> s l3 and l2

L4 503 L3 AND L2

=> s ((transfer(w)rna? or trna?) and (alanine or isoleucine) and chloroplast?)/a

L5 77 ((TRANSFER(W)RNA? OR TRNA?) AND (ALANINE OR ISOLEUCINE) AND CHLOROPLAST?)/AB,BI

=> s (gene or genes or vector? or plasmid? or cdna? or transgenic?)/ab,bi

L6 624232 (GENE OR GENES OR VECTOR? OR PLASMID? OR CDNA? OR TRANSGENIC?)/AB,BI

=> s l5 and l6

L7 64 L5 AND L6

=> s ((transfer(w)rna? or trna?) (l) (alanine or leucine))/ab,bi

L8 2086 ((TRANSFER(W)RNA? OR TRNA?) (L) (ALANINE OR LEUCINE))/AB,BI

=> s l8(l) (chloroplast?)/ab,bi

27670 (CHLOROPLAST?)/AB

32945 (CHLOROPLAST?)/BI

L9 85 L8 (L) (CHLOROPLAST?)/AB,BI

=> s l9 and l6

L10 57 L9 AND L6

=> s (spacer? or intergenic?)/ab,bi

L11 22205 (SPACER? OR INTERGENIC?)/AB,BI

=> s l10 and l11

L12 18 L10 AND L11

"PCT (IB 9.8/0499)"

PCT/6598/90423

59/078,640

CAS

BIOISI

6/15/88

Av 1638

FOX

=> file biosis

=> s 112

L13 2 L10 AND L11

=> dup remove

L14 20 DUP REMOVE L12 L13 (0 DUPLICATES REMOVED)

=> d 114 1-20

L14 ANSWER 1 OF 20 CA COPYRIGHT 1999 ACS

AN 123:107562 CA

TI Phylogenetic relationship of the green alga *Nanochlorum eukaryotum* deduced from its chloroplast rRNA sequences

AU Schreiner, M.; Geisert, M.; Oed, M.; Arendes, J.; Guengerich, U.; Breter, H.-J.; Stueber, K.; Weinblum, D.

CS Inst. Physiol. Chem. Pathobiochem., Johannes Gutenberg-Univ., Mainz, 55099, Germany

SO J. Mol. Evol. (1995), 40(4), 428-42

CODEN: JMEVAU; ISSN: 0022-2844

DT Journal

LA English

L14 ANSWER 2 OF 20 BIOSIS COPYRIGHT 1999 BIOSIS

AN 1995:339306 BIOSIS

DN PREV199598353606

TI Phylogenetic analysis of DNA sequence variation in the ***leucine***
tRNA ***gene*** group I intron of the ***chloroplast***
genome: An example from the Fabaceae.

AU Wojciechowski, Martin F. (1); Sanderson, Michael J.

CS (1) Dep. Ecol. Evolutionary Biol., Univ. Arizona, Tucson, AZ USA

SO American Journal of Botany, (1995) Vol. 82, No. 6 SUPPL., pp. 172.

Meeting Info.: 1995 Annual Meeting of the Botanical Society of America and the American Institute of Biological Sciences San Diego, California, USA August 6-10, 1995

ISSN: 0002-9122.

DT Conference

LA English

L14 ANSWER 3 OF 20 CA COPYRIGHT 1999 ACS

AN 115:65856 CA

TI Structural features of the plastid ribosomal RNA operons of two red algae: *Antithamnion* sp. and *Cyanidium caldarium*

AU Maid, Udo; Zetsche, Klaus

CS Inst. Pflanzenphysiol., Justus-Liebig-Univ., Giessen, D-6300, Fed. Rep. Ger.

SO Plant Mol. Biol. (1991), 16(4), 537-46

CODEN: PMBIDB; ISSN: 0167-4412

DT Journal

LA English

L14 ANSWER 4 OF 20 CA COPYRIGHT 1999 ACS

AN 115:152198 CA

TI Six group I introns and three internal transcribed ***spacers*** in the chloroplast large subunit ribosomal RNA ***gene*** of the green alga *Chlamydomonas eugametos*

AU Turmel, Monique; Boulanger, Jean; Schnare, Murray N.; Gray, Michael W.; Lemieux, Claude

CS Fac. Sci. Genie, Univ. Laval, Quebec, PQ, G1K 7P4, Can.

SO J. Mol. Biol. (1991), 218(2), 293-311

CODEN: JMOBAK; ISSN: 0022-2836

DT Journal

LA English

L14 ANSWER 5 OF 20 CA COPYRIGHT 1999 ACS

AN 114:179347 CA

TI Sequence analysis of the plastid rDNA ***spacer*** region of the chlorophyll c-containing alga *Cryptomonas* .PHI.

AU Douglas, Susan E.; Durnford, Dion G.

CS Atl. Res. Lab., Natl. Res. Counc., Halifax, NS, B3H 3Z1, Can.

SO DNA Sequence (1990), 1(1), 55-62

CODEN: DNSEES; ISSN: 1042-5179

DT Journal

LA English

L14 ANSWER 6 OF 20 CA COPYRIGHT 1999 ACS

AN 112:92847 CA

TI Chloroplast ribosomal DNA organization in the chromophytic alga *Olisthodiscus luteus*

AU Delaney, Terrence P.; Cattolico, Rose Ann

CS Dep. Bot., Univ. Washington, Seattle, WA, 98195, USA

SO Curr. Genet. (1989), 15(3), 221-9

CODEN: CUGED5; ISSN: 0172-8083

DT Journal

LA English

L14 ANSWER 7 OF 20 CA COPYRIGHT 1999 ACS

AN 109:223637 CA

TI Sequence of the plastid rDNA ***spacer*** region of the brown alga *Pylaiella littoralis* (L.) Kjellm. Evolutionary significance

AU Markowicz, Yves; Mache, Regis; Loiseaux-De Goer, Susan

CS Lab. Biol. Mol. Veg., Univ. Grenoble, Saint Martin d'Heres, F-38402, Fr.

SO Plant Mol. Biol. (1988), 10(5), 465-9

CODEN: PMBIDB; ISSN: 0167-4412

DT Journal

LA English

L14 ANSWER 8 OF 20 CA COPYRIGHT 1999 ACS

AN 111:34406 CA

TI Primary structure and sequence organization of the 16S - 23S ***spacer*** in the ribosomal operon of soybean (*Glycine max* L.) chloroplast DNA

AU De Lanversin, G.; Pillay, D. T. N.

CS Dep. Biol. Sci., Univ. Windsor, Windsor, ON, N9B 3P4, Can.

SO Theor. Appl. Genet. (1988), 76(3), 443-8

CODEN: THAGA6; ISSN: 0040-5752

DT Journal

LA English

L14 ANSWER 9 OF 20 CA COPYRIGHT 1999 ACS

AN 110:109254 CA

TI Structure and organization of *Marchantia polymorpha* chloroplast genome. I. Cloning and ***gene*** identification

AU Ohyama, Kanji; Fukuzawa, Hideya; Kohchi, Takayuki; Sano, Toru; Sano, Satoshi; Shirai, Hiromasa; Umesono, Kazuhiko; Shiki, Yasuhiko; Takeuchi, Masayuki; et al.

CS Fac. Agric., Kyoto Univ., Kyoto, 606, Japan

SO J. Mol. Biol. (1988), 203(2), 281-98

CODEN: JMOBAK; ISSN: 0022-2836

DT Journal

LA English

✓
ord
6/16

AA

✓
ord
6/16

- L14 ANSWER 10 OF 20 CA COPYRIGHT 1999 ACS
AN 109:1639 CA
TI Nucleotide sequence of the single ribosomal RNA operon of pea chloroplast DNA
AU Stummann, B. M.; Lehmbeck, J.; Bookjans, G.; Henningsen, K. W.
CS Dep. Genet., R. Vet. Agric. Univ., Frederiksberg, 1870, Den.
SO Physiol. Plant. (1988), 72(1), 139-46
CODEN: PHPLAI; ISSN: 0031-9317
DT Journal
LA English
- L14 ANSWER 11 OF 20 CA COPYRIGHT 1999 ACS
AN 108:181177 CA
TI Sequence studies on the soybean chloroplast 16S-23S rDNA ***spacer*** region. Comparison with other angiosperm sequences and proposal of a generalized RNA secondary structure model for the ***intergenic*** regions
AU De Lanversin, Guy; Pillay, Data T. N.; Jacq, Bernard
CS Dep. Biol., Univ. Windsor, Windsor, ON, N9B 3P4, Can.
SO Plant Mol. Biol. (1988), Volume Date 1987, 10(1), 65-82
CODEN: PMBIDB; ISSN: 0167-4412
DT Journal
LA English
- L14 ANSWER 12 OF 20 CA COPYRIGHT 1999 ACS
AN 108:181176 CA
TI Sequence organization of the chloroplast ribosomal ***spacer*** of Spinacia oleracea including the 3' end of the 16S rRNA and the 5' end of the 23S rRNA
AU Massenet, Oliver; Martinez, Pascal; Seyer, Patrick; Briat, Jean Francois
CS Lab. Biol. Mol. Veg., Univ. I Grenoble, Saint Martin d'Heres, F-38402, Fr.
SO Plant Mol. Biol. (1988), Volume Date 1987, 10(1), 53-63
CODEN: PMBIDB; ISSN: 0167-4412
DT Journal
LA English
- L14 ANSWER 13 OF 20 CA COPYRIGHT 1999 ACS
AN 104:201289 CA
TI Sequence organization of the chloroplast ribosomal ***spacer*** of Chlamydomonas reinhardtii: uninterrupted tRNA ile and tRNA ala ***genes*** and extensive secondary structure
AU Schneider, M.; Rochaix, J. D.
CS Dep. Mol. Biol. Plant Biol., Univ. Geneva, Geneva, 1211, Switz.
SO Plant Mol. Biol. (1986), 6(4), 265-70
CODEN: PMBIDB; ISSN: 0167-4412
DT Journal
LA English
- L14 ANSWER 14 OF 20 CA COPYRIGHT 1999 ACS
AN 103:65838 CA
TI The ***intergenic*** region between the Vicia faba chloroplast tRNACAALeu and tRNAUAALeu ***genes*** contains a partial copy of the split tRNACAALeu ***gene***
AU Bonnard, Geraldine; Weil, Jacques Henry; Steinmetz, Andre
CS Inst. Biol. Mol., Univ. Louis Pasteur, Strasbourg, F-67084, Fr.
SO Curr. Genet. (1985), 9(5), 417-22
CODEN: CUGED5; ISSN: 0172-8083
DT Journal
LA English
- L14 ANSWER 15 OF 20 CA COPYRIGHT 1999 ACS
AN 104:103260 CA
TI Structure of transfer RNA ***genes*** from broad bean (Vicia faba)

chloroplasts

AU Weil, J. H.; Bonnard, G.; Kuntz, M.; Michel, F.; Steinmetz, A.
 CS Inst. Biol. Mol. Cell., Univ. Louis Pasteur, Strasbourg, 67084, Fr.
 SO NATO ASI Ser., Ser. A (1985), 83 (Mol. Form Funct. Plant Genome), 313-24
 CODEN: NALSDJ
 DT Journal
 LA English

L14 ANSWER 16 OF 20 CA COPYRIGHT 1999 ACS
 AN 98:210711 CA
 TI Nucleotide sequence of a truncated rRNA operon of the Euglena gracilis
 chloroplast genome
 AU Roux, Etienne; Graf, Lucia; Stutz, Erhard
 CS Lab. Biochim., Univ. Neuchatel, Neuchatel, CH-2000, Switz.
 SO Nucleic Acids Res. (1983), 11(7), 1957-68
 CODEN: NARHAD; ISSN: 0305-1048
 DT Journal
 LA English

L14 ANSWER 17 OF 20 BIOSIS COPYRIGHT 1999 BIOSIS
 AN 1983:299437 BIOSIS
 DN BA76:56929
 TI THE ***GENE*** FOR A SPINACH ***CHLOROPLAST*** ISO ***LEUCINE***
 TRANSFER ***RNA*** HAS A METHIONINE ANTI CODON. ✓ ord 6/16
 AU KASHDAN M A; DUDOCK B S
 CS NEW ENGLAND NUCLEAR, 549 ALBANY ST., BOSTON, MASS. 02118.
 SO J BIOL CHEM, (1982) 257 (19), 11191-11194.
 CODEN: JBCHA3. ISSN: 0021-9258.
 FS BA; OLD
 LA English

L14 ANSWER 18 OF 20 CA COPYRIGHT 1999 ACS
 AN 96:194403 CA
 TI Euglena gracilis chloroplast transfer RNA transcription units. II.
 Nucleotide sequence analysis of a tRNAVal-tRNAAsn-tRNAArg-tRNALeu
 gene cluster
 AU Orozco, Emil M., Jr.; Hallick, Richard B.
 CS Dep. Chem., Univ. Colorado, Boulder, CO, 80309, USA
 SO J. Biol. Chem. (1982), 257(6), 3265-75
 CODEN: JBCHA3; ISSN: 0021-9258
 DT Journal
 LA English

L14 ANSWER 19 OF 20 CA COPYRIGHT 1999 ACS
 AN 97:18263 CA
 TI Nucleotide sequence of the 16S-23S ***spacer*** region in an rRNA
 gene cluster from tobacco chloroplast DNA ✓ ord 6/16
 AU Takaiwa, Fumio; Sugiura, Masahiro
 CS Natl. Inst. Genet., Mishima, 411, Japan
 SO Nucleic Acids Res. (1982), 10(8), 2665-76
 CODEN: NARHAD; ISSN: 0305-1048
 DT Journal
 LA English

L14 ANSWER 20 OF 20 CA COPYRIGHT 1999 ACS
 AN 93:233024 CA
 TI Euglena gracilis chloroplast ribosomal RNA transcription units. II.
 Nucleotide sequence homology between the 16S-23S ribosomal RNA
 spacer and the 16S ribosomal RNA leader regions
 AU Orozco, Emil M., Jr.; Rushlow, Keith E.; Dodd, Jesse R.; Hallick, Richard
 B.
 CS Dep. Chem., Univ. Colorado, Boulder, CO, 80309, USA
 SO J. Biol. Chem. (1980), 255(22), 10997-1103

DT Journal
LA English

=> d 120 1-14 ab

L20 NOT FOUND

The L-number entered has not been defined in this session, or it has been deleted. To see the L-numbers currently defined in this session, enter DISPLAY HISTORY at an arrow prompt (=>).

=> d 114 1-20 ab

L14 ANSWER 1 OF 20 CA COPYRIGHT 1999 ACS

AB The marine green coccoidal alga *Nanochlorum eukaryotum* (N.e.) is of small size with an av. diam. of 1.5 μ m. It is characterized by primitive-appearing biochem. and morphol. properties, which are considerably different from those of other green algae. Thus, it has been proposed the N.e. may be an early developed algal form. To prove this hypothesis, DNA of N.e. was isolated by a phenol extn. procedure, and the chloroplast DNA sepd. by preparative CsCl d.-gradient centrifugation. The kinetic complexity of the nuclear and the chloroplast DNA was evaluated by reassocn. kinetics to 3 .times. 107 bp and 9 .times. 104 bp, resp. Several chloroplast *****genes*****, including the rRNA *****genes*****, were cloned on distinct fragments. The order of the rRNA *****genes***** corresponds to the common prokaryotic pattern. The 16S rRNA *****gene***** comprises 1,548 bases and is sepd. from the 23S rRNA *****gene***** with its 2,920 bases by a short *****spacer***** of 460 bases, which also includes the tRNA^{Ile} and tRNA^{Ala} *****genes*****. The 5S rRNA *****gene***** has not been found; it must start further than 500 bases downstream from the 3'-end of the 23S rRNA *****gene*****. From the chloroplast rRNA sequences, we have deduced secondary structures of the 16S and 23S rRNAs, which are in agreement with std. models. The rRNA sequences were aligned with corresponding chloroplast sequences; phylogenetic relationships were calcd. by several methods. From these calcns., we conclude that N.e. is most closely related to *Chlorella vulgaris*. Therefore, N.e. does not represent an early developed algal species; the primitive-appearing morphol. and biochem. characteristics of N.e. must rather be explained by secondary losses.

L14 ANSWER 2 OF 20 BIOSIS COPYRIGHT 1999 BIOSIS

L14 ANSWER 3 OF 20 CA COPYRIGHT 1999 ACS

AB The nucleotide sequence of the plastid 16S rDNA of the multicellular red alga *Antithamnion* sp. and the 16S rDNA/23S rDNA *****intergenic***** *****spacers***** of the plastid DNAs of the unicellular red alga *C. caldarium* and of *Antithamnion* sp. were detd. Sequence comparisons support the idea of a polyphyletic origin of the red algal and the higher-plant chloroplasts. Both *****spacer***** regions include the unsplit tRNA^{Ile}(GAU) and tRNA^{Ala}(UGC) *****genes***** and so the plastids of both algae form a homogeneous group with those of chromophytic algae and *Cyanophora paradoxa* characterized by small-sized rDNA *****spacers***** in contrast to green algae and higher plants. Nevertheless, remarkable sequence differences within the rRNA and the tRNA *****genes***** gives the plastids of *C. caldarium* a rather isolated position.

L14 ANSWER 4 OF 20 CA COPYRIGHT 1999 ACS

AB The chloroplast large subunit rRNA *****gene***** of *C. eugametos* and its 5' flanking region encoding tRNA^{Ile}(GAU) and tRNA^{Ala}(UGC) have been sequenced. The DNA sequence data along with the results of a detailed RNA anal. disclosed 2 unusual features of this green algal large subunit rRNA *****gene*****: (1) the presence of 6 group I introns (CeLSU.cntdot.1-

CeLSU.cntdot.6) whose insertion positions have not been described previously, and (2) the presence of 3 short internal transcribed *****spacers***** that are post-transcriptionally excised to yield 4 rRNA species of 280, 52, 810 and 1720 nucleotides, positioned in this order (5' to 3') in the primary transcript. Together, these RNA species can assume a secondary structure that is almost identical to that proposed for the 23 S rRNA of *Escherichia coli*. All 3 internal transcribed *****spacers***** map to variable regions of primary sequence and (or) potential secondary structure, whereas all 6 introns lie within highly conserved regions. The first 3 introns are inserted within the sequence encoding the 810-nucleotide rRNA species and map within domain II of the large subunit rRNA structure; the remaining introns, found in the sequence encoding the 1720-nucleotide rRNA species, lie within either domain IV or V, as is the case for all other large subunit rDNA introns that have been documented to date. CeLSU.cntdot.5 and CeLSU.cntdot.6 each contain a long open reading frame (ORF) of more than 200 codons. While the CeLSU.cntdot.6 ORF is not related to any known ORFs, the CeLSU.cntdot.5 ORF belongs to a family of ORFs that have been identified in *Podospira* and *Neurospora* mitochondrial group I introns. The finding that a polymorphic marker showing unidirectional *****gene***** conversion during crosses between *C. eugametos* and *C. moewusii* is located within the CeLSU.cntdot.5 ORF makes it likely that this intron is a mobile element and that its ORF encodes a site-specific endonuclease promoting the transfer of the intron DNA sequence.

L14 ANSWER 5 OF 20 CA COPYRIGHT 1999 ACS

AB A 0.8-kb *AvaI*/*SmaI* fragment of the plastid genome of the chlorophyll c-contg. alga *Cryptomonas .PHI.* encompassing the rRNA *****spacer***** region and flanking *****genes***** was cloned and sequenced. The *****spacer***** region between the 16 S and 23 S rRNA *****genes***** is 275 bp long, one of the shortest yet reported, and it contains uninterrupted *****genes***** for tRNA^{Ile} and tRNA^{Ala} sepd. by only 2 bp. The coding regions for tRNAs and rRNAs were compared with those from cyanobacteria, land plants, and other algae and the possible evolutionary relationships discussed.

L14 ANSWER 6 OF 20 CA COPYRIGHT 1999 ACS

AB There are almost no data describing chloroplast genome organization in chromophytic (chlorophyll a/c) plants. In this study, chloroplast ribosomal operon placement and *****gene***** organization has been detd. for the golden-brown alga *O. luteus*. RRNA *****genes***** are located on the chloroplast DNA inverted repeat structure. Nucleotide sequence anal. demonstrated that in contrast to the larger *****spacer***** regions in land plants, the 16S-23S rDNA *****spacer***** of *O. luteus* is only 265 bp in length. This *****spacer***** contains tRNA^{Ile} and tRNA^{Ala} *****genes***** which lack introns and are sepd. by only 3 bp. The sequences of the tRNA *****genes***** and 16S and 23S rDNA termini flanking the *****spacer***** were examd. to det. homol. between *O. luteus*, chlorophytic plant chloroplast DNA, and prokaryotes.

L14 ANSWER 7 OF 20 CA COPYRIGHT 1999 ACS

AB The DNA segment situated between the 16 S and 23 S rRNA *****genes***** belonging to the plastid genome of the brown alga *Pylaiella littoralis* (L.) Kjellm. was sequenced. This small region consisting of 322 base pairs (bp) contains 2 unsplit tRNA *****genes***** sepd. by 3 bp. A comparison with similar regions from different plants shows that this region has evolved in 2 different ways according to the location of plants in evolutionary history. In the primitive group, this region is reduced in size when compared to prokaryotes. In the other groups, it is considerably enlarged by insertion of repetitive sequences, open reading frames and introns.

L14 ANSWER 8 OF 20 CA COPYRIGHT 1999 ACS

AB The nucleotide sequence of a ***spacer*** region between 16S and 23S rRNA ***genes*** from soybean chloroplasts was detd. The ***spacer*** region is over 3000 bp long and contains two tRNA ***genes***, coding for tRNA^{Ile} and tRNA^{Ala}, which contain intervening sequences of 953 and 811 base pairs, resp. There is a strong homol. between the two introns, suggesting that they have a common origin. These ***spacer*** tRNAs are synthesized as part of a kb precursor mol. contg 16S and 23S rRNA sequences.

L14 ANSWER 9 OF 20 CA COPYRIGHT 1999 ACS

AB The complete nucleotide sequence of chloroplast DNA from a liverwort, *M. polymorpha*, was detd. using a clone bank of chloroplast DNA fragments. The circular genome consists of 121,024 base-pairs and includes two large inverted repeats (IRA and IRB, each 10,058 base-pairs), a large single-copy region (LSC, 81,095 base-pairs), and a small single-copy region (SSC, 19,813 base-pairs). The nucleotide sequence was analyzed with a computer to deduce the entire ***gene*** organization, assuming the universal genetic code and the presence of introns in the coding sequences. It detected 136 possible ***genes***, 103 ***gene*** products of which are related to known stable RNA or protein mols. Stable RNA ***genes*** for four species of rRNA and 32 species of tRNA were located, although one of the tRNA ***genes*** may be defective. Twenty ***genes*** encoding polypeptides involved in photosynthesis and electron transport were identified by comparison with known chloroplast ***genes***. Twenty-five open reading frames (ORFs) show structural similarities to *Escherichia coli* RNA polymerase subunits, 19 ribosomal proteins and two related proteins. Seven ORFs are comparable with human mitochondrial NADH dehydrogenase ***genes***. A computer-aided homol. search predicted possible chloroplast homolog of bacterial proteins; two ORFs for bacterial 4Fe-4S-type ferredoxin, two for distinct subunits of a protein-dependent transport system, one ORF for a component of nitrogenase, and one for an antenna protein of a light-harvesting complex. The other 33 ORFs, consisting of 29 to 2136 codons, remain to be identified, but some of them seem to be conserved in evolution. There may be 22 introns in 20 ***genes*** (8 tRNA ***genes*** and 12 ORFs), which may be classified into the groups I and II found in fungal mitochondrial ***genes***. The structural ***gene*** for ribosomal protein S12 is trans-split on the opposite DNA strand. The universal genetic code was confirmed by the substitution pattern of simultaneous codons, and by possible codon recognition of the chloroplast-encoded tRNA mols., assuming no importation of tRNA mols. from the cytoplasm. The nucleotide residue A or T is preferred at the third position of the codons (G + C, 11.9%) and in ***intergenic*** ***spacers*** (G + C, 19.5%), resulting in an overall G + C content that is low (28.8%) throughout the liverwort chloroplast genome. Possible ***gene*** expression signals such as promoters and terminators for transcription, predicted locations of ***gene*** products, and DNA replicative origins are discussed.

L14 ANSWER 10 OF 20 CA COPYRIGHT 1999 ACS

AB The nucleotide sequence of an 8-kbp region of pea (*Pisum sativum*) chloroplast DNA contg. the rRNA operon and putative promoter sites was detd. and compared to the corresponding sequences from maize, tobacco, and the liverwort *Marchantia polymorpha*. The chloroplast DNA species of all vascular plants investigated, with the exception of a few legumes including pea, and of *Marchantia* contain an inverted repeat with an rRNA operon. The pea rRNA operon is the first sequenced rRNA operon from a plant with only 1 copy of the rRNA ***genes*** per mol. of chloroplast DNA. The organization of the operon is the same as for maize, tobacco and *Marchantia*, i.e., tRNA-Val ***gene*** /16 S rRNA ***gene*** / ***spacer*** with intron-contg. ***genes*** for tRNA-Ile and tRNA-Ala/23 S rRNA ***gene*** /4.5 S rRNA ***gene*** /5 S rRNA ***gene***. Current evidence suggests that the tRNA-Val

gene may not be cotranscribed with the other ***genes***. The pea 16 S, 23 S, 4.5 S and 5 S rRNA have 1488, 2813, 105, and 121 nucleotides, resp. The homologies of the entire operon (the tRNA-Val ***gene*** - 5 S rRNA region) to those from tobacco, maize, and Marchantia are 88, 82, and 79%, resp. The corresponding homologies for tobacco/maize, tobacco/Marchantia and maize/Marchantia have similar values. The 16 S and 23 S rRNA ***genes*** from pea are >90% homologous to those from the 3 other species. The fact that pea only has 1 set of rRNA ***genes*** per mol. chloroplast DNA is apparently not correlated with any significant difference between the pea operon and the rRNA operons from tobacco, maize, and Marchantia.

L14 ANSWER 11 OF 20 CA COPYRIGHT 1999 ACS

AB The sequence of the ribosomal ***spacer*** region of soybean chloroplast DNA including the 3' end of the 16 S rRNA ***gene***, the tRNAAla and tRNAIle ***genes*** (but not their introns), the 3 ***intergenic*** regions, and the 5' end of the 23 S rRNA ***gene***, was detd. This sequence has been compared to corresponding regions of other angiosperm chloroplast DNAs. Secondary structure models are proposed for the entirety of the ***intergenic*** regions a, b, and c and for the flanking rRNA regions. A model for a common secondary structure of the ribosomal ***spacer*** ***intergenic*** regions from chloroplasts of higher plants is proposed, which is supported by comparative evidence.

L14 ANSWER 12 OF 20 CA COPYRIGHT 1999 ACS

AB The 2201-bp ***spacer*** between the chloroplast ribosomal 16 S and 23 S ***genes*** of *S. oleracea* was sequenced. It contains the ***genes*** of the tRNAIle (GAU) and tRNAAla (UGC) which are both interrupted by introns of 728 and 816 bp, resp. These introns belong to the class II. Comparison of the rRNA-specifying DNA ***spacer*** sequence of maize, tobacco, and spinach indicates that no conserved polypeptide is encoded within the introns of the 2 tRNA ***genes*** and that the 2 main insertions/deletions between the 3 plants are located within 2 loops of the class II introns secondary structure, which is therefore conserved. Based on the sequence complementarity obsd. between the upstream and downstream parts, of the 16 S and 23 S rRNA ***genes***, RNase III-like secondary structures involved in the processing of the rRNA precursor are proposed.

L14 ANSWER 13 OF 20 CA COPYRIGHT 1999 ACS

AB The 1805-base-pair (bp) ***spacer*** between the chloroplast ribosomal 16 S and 7 S RNA ***genes*** of *C. reinhardtii* was sequenced. It contains the ***genes*** of tRNA ala and tRNA ile which are both uninterrupted. The ***spacer*** includes several short direct and inverted repeats and a large palindromic structure which maps in the region where DNA rearrangements have occurred in other *Chlamydomonas* species.

L14 ANSWER 14 OF 20 CA COPYRIGHT 1999 ACS

AB A cluster of 3 tRNA ***genes*** located on fragment Bam6a from *V. faba* chloroplast DNA was sequenced; it contains the ***genes*** for tRNACAALeu, tRNAUAALeu, and tRNAPhe. The 2 tRNALeu ***genes*** are sepd. by 443 base pairs (bp) and are transcribed divergently from different DNA strands. The ***intergenic*** region contains a series of short repeats and a partial copy of the split tRNAUAALeu ***gene*** which includes 100 bp of the 5' flanking region, 35 bp of the 5' exon, and the 1st 42 bp of the intron. It is possible that some of these duplications occurred upon the rearrangement of the 2 tRNALeu ***genes*** in broad bean (and in pea) or upon the deletion of 1 copy of the inverted repeat, since in all other higher plant chloroplast genomes studied so far these 2 tRNALeu ***genes*** are located far apart on the genome, 1 being in the inverted repeat region, the other being in the

large single copy region. The tRNAPhe and tRNAUAALeu are encoded by the same DNA strand and are sepd. by 110 bp.

L14 ANSWER 15 OF 20 CA COPYRIGHT 1999 ACS

AB The fine-structure organization and nucleotide sequences of 6 broad bean chloroplast tRNA ***genes*** and ***intergenic*** regions were studied. The ***genes*** for 2 of the tRNAs, tRNA^{Leu}(CAA) and tRNA^{Leu}(UAA), which generally are located far apart on most chloroplast genomes, were found close together in the broad bean genome. The ***intergenic*** region has a series of short direct repeats and a partial duplication of 1 of these ***genes***. None of the 6 chloroplast tRNA ***genes*** studied encodes the 3'-terminal CCA sequence; this sequence, which is present in mature tRNAs, has to be added posttranscriptionally.

L14 ANSWER 16 OF 20 CA COPYRIGHT 1999 ACS

AB An extra 16 S rRNA ***gene*** (s-16 S rDNA) from the *E. gracilis* ***chloroplast*** genome and several hundred positions of its flanking regions were sequenced. The structural part has 1486 positions and is 98% homologous in its sequence with the 16 S rRNA ***gene*** in functional ***chloroplast*** rRNA operons. Sequences of approx. 200 positions upstream and 15 positions downstream of the structural part of the s-16 S rRNA ***gene*** region are highly homologous with corresponding parts in the functional operon. Neither ***tRNA*** ***genes*** (***alanine***, isoleucine) nor parts of the 23 S and 5 S rRNA ***genes*** are found within 557 positions after the 3' end of the s-16 S rRNA ***gene***; i.e., the 300-base-pair homol. obsd. in electron microscopic studies of heteroduplexes between the s-16S rDNA downstream region and the 6.2-kilobase repeated segment contg. the functional rRNA operon must be due to a DNA stretch in the interoperon ***spacer***. A structural model of the truncated rRNA operon is presented. S-1 endonuclease anal. indicated that the s-16 S rDNA region is probably not transcribed into stable s-16 S rRNA.

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AB The nucleotide sequence of the ***gene*** for spinach chloroplast tRNA^{Ile} was determined. The ***gene*** is found in 2 copies located in the inverted repeat regions of spinach chloroplast DNA, but not within the rRNA ***spacer***. Both copies of the tRNA^{Ile} ***gene*** were sequenced and found to be identical. A very unusual characteristic of the tRNA^{Ile} ***gene*** is that the anticodon is CAT, which is a methionine anticodon. In the tRNA, the C residue in the anticodon is subsequently modified, presumably to prevent misreading of the genetic code. The spinach chloroplast tRNA^{Ile} ***gene*** is colinear with its RNA sequence and does not contain an intervening sequence, as has been reported for maize chloroplast tRNA^{2Ile}. The tRNA^{Ile} ***gene*** does not code for the 3'-terminal CCA end, nor do any other tRNA ***genes*** appear to be contiguous with this ***gene***.

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AB The tRNA-coding locus of the 8.2-kilobase-pair (kbp) EcoRI fragment Eco G of *E. gracilis* chloroplast DNA was chosen for detailed anal. Two recombinant ***plasmids***, pPG14 (contg. Eco G and the ***vector*** pMB9) and pEZC23 (contg. the chloroplast DNA fragment HindIII B cloned in ***plasmid*** pBR322) were employed. The tRNA locus was mapped to an 0.8-kbp region of Eco G also present in the HindIII B. The DNA sequence of a 1.6-kbp fragment from HindIII B, which contained the entire tRNA ***gene*** locus, was detd. Four tRNA ***genes*** were identified from the DNA sequence. The ***gene*** organization is tRNA^{Val}-(16-bp ***spacer***)-tRNA^{Asn}-(3-bp ***spacer***)-tRNA^{Arg}-(45-bp ***spacer***)-tRNA^{Leu}. The tRNA^{Leu} ***gene*** is of the opposite polarity from the other 3 ***genes***. This is the 1st evidence of such a tRNA cluster for a chloroplast genome. Also evident from the DNA

sequence, 132 bp from the 5'-end of the tRNA^{Leu} ***gene***, is a putative ***gene*** or pseudogene for a chloroplast protein.

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AB The nucleotide sequence of a ***spacer*** region between 16 S and 23 S rRNA ***genes*** from tobacco chloroplasts has been detd. The ***spacer*** region is 2080 base-pairs (bp) and encodes tRNA^{Ile} and tRNA^{Ala} ***genes*** which contain intervening sequences of 707 bp and 710 bp, resp. Strong homol. between the 2 intervening sequences is obsd. These ***spacer*** tRNAs are synthesized as part of an 8.2-kilobase precursor mol. contg. 16 S and 23 S rRNA sequences.

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AB The DNA sequences of 2 segments of the rRNA transcription units of *E. gracilis* Pringsheim strain Z chloroplast DNA were detd. The 1st is from the 16 S to 23 S rRNA ***spacer*** region. The nucleotide sequence detd. includes 64 base pairs (bp) from the 3'-end of the 16 S rRNA ***gene***, the adjacent 87-bp ***spacer*** contg. 68 A-T base pairs, a tRNA^{Ile} ***gene***, a 9-bp ***spacer***, a tRNA^{Ala} ***gene***, a ***spacer*** of .apprx.15 bp, and the 1st 120 bp from the 5'-end of the 23 S rRNA ***gene***. The ***gene*** organization of the 16 S to 23 S rRNA ***spacer***, the identity of the tRNA ***genes***, and the tRNA anticodons for the *E. gracilis* rRNA transcription units are identical with that of the rrnA, D, and X operons of *Escherichia coli*. The 2nd DNA segment which was sequenced is from a region preceding the 5'-end of the 16 S rRNA ***gene***. Within a continuous region of 189 bp in this 16 S rRNA leader sequence, 68% of the bases are homologous to the 16 S rRNA to 23 S rRNA ***spacer*** region. This homol. includes the 3'-end of the 16 S rRNA ***gene***, the adjacent ***spacer***, and a complete pseudo tRNA^{Ile} ***gene***. This leader sequence which has the same polarity as the rRNA transcripts, is flanked by nucleotide sequences resembling partial tRNA ***genes***.

=> log y

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